RAW SEQUENCE LISTING PATENT APPLICATION US/08/468,161

DATE: 07/13/95 TIME: 17:50:25

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQ	JENCE LISTING	
2 3	(1) G	eneral Information:		
4	(1)	eneral informacion.		
5 6 7 8	(i)	APPLICANT: DeFeo-Jones, Debe Feng, Dong-Mei Garsky, Victor M Jones, Raymond E	•	ENTERED
9		Oliff, Allen I.		
10				
11	(11)	TITLE OF INVENTION: NOVEL P	EPTIDES	
12 13	/ 4 4 4 4 1	NUMBER OF SEQUENCES: 146		
14	(111)	NUMBER OF SEQUENCES: 146	<u>.</u>	
15	(iv)	CORRESPONDENCE ADDRESS:	·	
16	(,	(A) ADDRESSEE: DAVID A. MU	THARD	
17		(B) STREET: 126 E. Lincoln		00
18		(C) CITY: RAHWAY		
19		(D) STATE: NEW JERSEY		
20		(E) COUNTRY: U.S.A.		
21		(F) ZIP: 07065		
22 23	(**)	COMPUTER READABLE FORM:		
23 24	(∨)	(A) MEDIUM TYPE: Floppy dis	≥ ŀ	•
25		(B) COMPUTER: IBM PC compat		
26		(C) OPERATING SYSTEM: PC-DO		
27		(D) SOFTWARE: PatentIn Rele		1.30
28				
29	(vi)	CURRENT APPLICATION DATA:		
30		(A) APPLICATION NUMBER:		
31		(B) FILING DATE:		
32		(C) CLASSIFICATION:		
33 34	(********	ATTORNEY/AGENT INFORMATION:		
35	(\(\frac{1}{1} \)	(A) NAME: Muthard, David A		
36		(B) REGISTRATION NUMBER: 3		
37		(C) REFERENCE/DOCKET NUMBER	•	
38		(, ,		
39	(ix)	TELECOMMUNICATION INFORMATIO	ON:	
40		(A) TELEPHONE: (908)594-390)3	•
41		(B) TELEFAX: (908)594-4720		
42				
43				
44	(2) INFO	RMATION FOR SEQ ID NO:1:		
45 46	/ 4 \	CENTENCE CUADACMEDICATOS.		
40	(1)	SEQUENCE CHARACTERISTICS:		

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													ALVA	U A D	LI. U	7//7.
47 48 49		(A) LENGTH: 462 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single														
50 51		•	(D) TOPOLOGY: linear													
52 53	(ii)	MOL	MOLECULE TYPE: peptide													
54 55	(iii)	НУР	HYPOTHETICAL: NO													
56 57	(iv)	ANT	ANTI-SENSE: NO													
58 59	(V)	FRA	FRAGMENT TYPE: internal													
60 61 62									·							
63 64	(xi)	SEQ	SEQUENCE DESCRIPTION: SEQ ID NO:1:													
65 66	Met 1	Lys	Pro	Asn	Ile 5	Ile	Phe	Val	Leu	Ser 10	Leu	Leu	Leu	Ile	Leu 15	Glu
67 68 69	Lys	Gln	Ala	Ala 20	Val	Met	Gly	Gln	Lys 25	Gly	Gly	Ser	Lys	Gly 30	Arg	Leu
70 71 72	Pro	Ser	Glu 35	Phe	Ser	Gln	Phe	Pro	His	Gly	Gln	Lys	Gly 45	Gln	His	Tyr
73 74	Ser	_	Gln	Lys	Gly	Lys			Thr	Glu	Ser	_	Gly	Ser	Phe	Ser
75 76 77	Tla	50	Tyr	mb ~	M	ui a	55 Val	ð an	. הוג	Acn	A c n	60	A a w	al n	Sor	Ara
78 79	65	GIII	ıyı	1111	ıyı	70	Val	АБР	ATG	ASII	75	nis	АЗР	GIII	Ser	80
80 81	Lys	Ser	Gln	Gln	Tyr 85	Asp	Leu	Asn	Ala	Leu 90	His	Lys	Thr	Thr	Lys 95	Ser
82 83 84 85	Gln	Arg	His	Leu 100	Gly	Gly	Ser	Gln	Gln 105	Leu	Leu	His	Asn	Lys 110	Gln	Glu
86 87 88	Gly	Arg	Asp 115	His	Asp	Lys	Ser	Lys 120	Gly	His	Phe	His	Arg 125	Val	Val	Ile
89 90 91	His	His 130	Lys	Gly	Gly	Lys	Ala 135	His	Arg	Gly	Thr	Gln 140	Asn	Pro	Ser	Gln
92 93 94	Asp 145	Gln	Gly	Asn	Ser	Pro 150	Ser	Gly	Lys	Gly	Ile 155	Ser	Ser	Gln	Tyr	Ser 160
95 96 97	Asn	Thr	Glu	Glu	Arg 165	Leu	Trp	Val	His	Gly 170	Leu	Ser	Lys	Glu	Gln 175	Thr
98 99	Ser	Val	Ser	Gly 180	Ala	Gln	Lys	Gly	Arg 185	Lys	Gln	Gly	Gly	Ser 190	Gln	Ser

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100 101	Sor	Tyr	Val	Ι.Δ11	Gln	Thr	Glu	Glu	T.011	Va1	Δla	Aen	T.ve	Gln	Gln	Δra
102	Der	1 y 1	195	nea	OIII		OIG	200	пеа	VGI	ALG	ASII	205	0111	U 111	n. g
103																
104	Glu	Thr	Lvs	Asn	Ser	His	Gln	Asn	Lys	Glv	His	Tyr	Gln	Asn	Val	Val
105		210					215					220				
106																
107	Glu	Val	Arg	Glu	Glu	His	Ser	Ser	Lys	Val	Gln	Thr	Ser	Leu	Cys	Pro
108	225					230			•		235				•	240
109																
110	Ala	His	Gln	Asp	Lys	Leu	Gln	His	Gly	Ser	Lys	Asp	Ile	Phe	Ser	Thr
111					245					250					255	
112																
113	Gln	Asp	Glu	Leu	Leu	Val	Tyr	Asn	Lys	Asn	Gln	His	Gln	Thr	Lys	Asn
114				260					265					270		
115																
116	Leu	Asn		Asp	Gln	Gln	His	_	Arg	Lys	Ala	Asn	Lys	Ile	Ser	Tyr
117			275					280					285			
118	_						-								_	
119	Gln	Ser	Ser	Ser	Thr	Glu		Arg	Arg	Leu	His	_	Gly	Glu	Asn	GTÀ
120		290					295					300				
121		~1	•	•	7	a	a1	~	a	-1-	m	a	a1	m1	a1	a1
122		Gln	rys	Asp	vaı		GIN	Ser	Ser	тте		Ser	GIn	Thr		
123	305					310					315					320
124	T	Ala	a1 n	a1	T	C0*	01 n	T ***	a1 n	т1.	mb ~	T1.	Dro	802	01 n	01 11
125 126	rhs	АТА	GIII	СТУ	325	Ser	GIII	пåэ	GIII	330	1111	TTE	FIU	per	335	GIU
127					323				•	330					333	
128	Gln	Glu	His	Ser	Gln	I.vs	Δla	Δsn	I.vs	Tle	Ser	Tur	Gln	Ser	Ser	Ser
129	01	014		340	01	_,_			345		501	- 7 -		350		201
130																
131	Thr	Glu	Glu	Arq	Arq	Leu	His	Tyr	Gly	Glu	Asn	Gly	Val	Gln	Lys	Asp
132			355	_				360	-			-	365		-	-
133																
134	Val	Ser	Gln	Arg	Ser	Ile	Tyr	Ser	Gln	Thr	Glu	Lys	Leu	Val	Ala	Gly
135		370					375					380				
136																
137	_	Ser	Gln	Ile	Gln		Pro	Asn	Pro	Lys		Glu	Pro	Trp	His	_
138	385					390					395					400
139		_		_			_			_		_	_			_
140	Glu	Asn	Ala	Lys	GTA	GLu	Ser	СТĀ				Asn	Arg	GIU		Asp
141					405					410					415	
142	T	T		77.5	a1	a1	r	a 1	3	**1 _	a1	774	a1	a	772	G1
143	Leu	Leu	ser		GIU	GIN	ràs	сту	_	HIS	GIN	HIS	GIY		HIS	GIA
144 145				420					425					430		
145	al ••	Leu	y en	Tla	Va1	Tle	Tle	@1 11	Gl n	al	λer	λen	Ser	λen	Δτα	Hie
145	СТУ	ьeu	435	TTG	Val	TTG	TTG	440	GTII	GIU	vəħ	тор	445	чэр	AL Y	1112
148			-33					740					7 T J			
149	T.e.11	Ala	Gln	His	T.eu	Asn	Asn	Asp	Ara	Asn	Pro	Leu	Phe	Thr		
150	neu .	450	O T 11		Leu	2.011	455	p	*** 9		- 10	460				
151		-50														
152	(2) INFO	RMAT:	ION I	OR S	SEO I	D NO	0:2:									
-	, = , = ====															

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153
           (i) SEQUENCE CHARACTERISTICS:
154
155
                (A) LENGTH: 15 amino acids
                (B) TYPE: amino acid
156
157
                (C) STRANDEDNESS: single
158
                (D) TOPOLOGY: linear
159
          (ii) MOLECULE TYPE: peptide
160
161
162
         (iii) HYPOTHETICAL: NO
163
          (iv) ANTI-SENSE: NO
164
165
166
           (v) FRAGMENT TYPE: internal
167
168
169
170
171
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
172
           Gly Lys Gly Ile Ser Ser Gln Tyr Ser Asn Thr Glu Glu Arg Leu
173
174
175
     (2) INFORMATION FOR SEQ ID NO:3:
176
177
           (i) SEQUENCE CHARACTERISTICS:
178
179
                (A) LENGTH: 11 amino acids
180
                (B) TYPE: amino acid
181
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
182
183
          (ii) MOLECULE TYPE: peptide
184
185
186
         (iii) HYPOTHETICAL: NO
187
188
          (iv) ANTI-SENSE: NO
189
190
           (v) FRAGMENT TYPE: internal
191
192
193
194
195
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
196
197
          Asn Lys Ile Ser Tyr Gln Ser Ser Ser Thr Glu
198
                           5
           1
199
200
     (2) INFORMATION FOR SEQ ID NO:4:
201
           (i) SEQUENCE CHARACTERISTICS:
202
203
                (A) LENGTH: 19 amino acids
204
                (B) TYPE: amino acid
205
                (C) STRANDEDNESS: single
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206
                (D) TOPOLOGY: linear
207
208
          (ii) MOLECULE TYPE: peptide
209
         (iii) HYPOTHETICAL: NO
210
211
212
          (iv) ANTI-SENSE: NO
213
214
           (v) FRAGMENT TYPE: internal
215
216
217
218
219
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
220
221
           Gly Glu Asn Gly Val Gln Lys Asp Val Ser Gln Arg Ser Ile Tyr Ser
222
                                                 10
                                                                      15
223
224
           Gln Thr Glu
225
226
227
      (2) INFORMATION FOR SEQ ID NO:5:
228
229
           (i) SEQUENCE CHARACTERISTICS:
230
                (A) LENGTH: 19 amino acids
231
                (B) TYPE: amino acid
232
                (C) STRANDEDNESS: single
233
                (D) TOPOLOGY: linear
234
          (ii) MOLECULE TYPE: peptide
235
236
237
         (iii) HYPOTHETICAL: NO
238
239
          (iv) ANTI-SENSE: NO
240
           (v) FRAGMENT TYPE: internal
241
242
243
244
245
246
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
247
248
           Gly Glu Asn Gly Val Gln Lys Asp Val Ser Gln Ser Ser Ile Tyr Ser
249
250
251
           Gln Thr Glu
252
253
254
      (2) INFORMATION FOR SEQ ID NO:6:
255
256
           (i) SEQUENCE CHARACTERISTICS:
257
                (A) LENGTH: 25 amino acids
                (B) TYPE: amino acid
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/468,161

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